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Minimum
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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7.2	7.2	7.2	7.2	7.2	7.2	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.5	7.5	7.5	7.5
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Q63731 rattus norv	Q9gjp9 oryctolagus	Q914n1 streptococc	7	Q90yf6 paracirrhit		Q99mil mus musculu	Q9amc4 streptococc	096063 dugesia jap	Q98tq5 notothenia		P87344 theragra ch	Q9ups1 homo sapien		Q9qz84 mus musculu	6 no	S						Q9fj35 arabidopsis		homo saj		1	276 caeno	Q9y577 homo sapien

ALIGNMENTS

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Best Local Similarity 100.0%;
Matches 469; Conservative (
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01-JUL-1997
01-DEC-2001
                                                                                                                                                                     EMBL; U77845; AAB52993.1; -.
Interpro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                          000467
                                                                                                              Zinc-finger.
SEQUENCE 4
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                             HTRIP.
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                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                       HTRIP.
                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
 61 KLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVS 120
                                MPIRALCTICSDFFDHSRDVAAIHCGHTFHLQCLIQSFETAPSRTCPQCRIQVGKRTIIN
                    MPIRALCTICSDFFDHSRDVAAIHCGHTFHLQCLIQSFETAPSRTCPQCRIQVGKRTIIN
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                                                                                                              53138 MW;
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Last sequence update)
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                                                                      Score 2384; DB 4; Pred. No. 1.7e-121;
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                                                                                                              2D54ED04B84ABAE4 CRC64;
                                                             Mismatches
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Q9BWF2;
Q9BWF2;
01-JUN-2001 (TrEMBLrel. 17, C:
01-JUN-2001 (TrEMBLrel. 17, L:
01-DEC-2001 (TrEMBLrel. 19, L:
TRAF INTERRACTING PROTEIN.
                                                                                                                                                                                                            Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBar Submitted (NOV-2000) to the EMBL/GenBar i - SIMILARITY: CONTAINS 1 RING-TYPE Z1 EMBL; BC000310; AAH00310.1; - I EMBL; BC000310; AAH00310.1; - I PRO001841; Znf_ring. Pfam; PF00097; Zf-C3H44; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammaila; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                             Zinc-finger.
SEQUENCE 4
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LQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEARRLRSKMKTMEQIELLLQSQRPEV
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                                                                                 KLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVS
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Last sequence update)
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                                                                                                                                               Score 2357; I
Pred. No. 4.86
0; Mismatches
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RX MEDILINE-21085660; pubMed-11217851;
RA MARCHINE-21085660; pubMed-11217851;
RA ALCARWA J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Alcawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alcawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alcawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alcawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Casavant T.,
RA Alcawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Basole G., Quackenbush J.,
RA Kitoh P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Kochida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
Ra Hayashizaki Y.,
Ra Hayashizaki Y.,
Ra Hayashizaki Y.,
Query Match 78.5
Best Local Similarity 79.1
Matches 370; Conservative
                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA Nature 409:685-690(2001).

-i-SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
EMBL; AK012948; BAB28567.1; -.
EMBL; AK012786; BAB28469.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
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                                                                                                        Zinc-finger.
SEQUENCE 4
                                                                                                                                                                    MGD; MGI:1096377; Traip.
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
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                                                                                                                                               SM00184; RING;
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                     78.5%;
79.1%;
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Last sequence update)
Last annotation update)
Score 1870.5; DB 11;
Pred. No. 9.2e-94;
2; Mismatches 55; 1
                                                                                                          EBFABC49A9F4BF2E CRC64;
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MEDLINE=97258620; PubMed=9104814;

A Lee S.Y., Lee S.Y., Choi Y.;

MEDLINE=97258620; PubMed=9104814;

Therefore receptor (TNFR)- and CD30-TRAF signaling complication of the tume of the time of time of the time of time of the time of the time of time of time of the time of time of the time of t
                                                                                                                                        Query Match 77.5%;
Best Local Similarity 78.4%;
Matches 367; Conservative
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008854;
01-JUL-1997
01-JUL-1997
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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KLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVES
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Rodentia;
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                                                                                                                                        Score 1847.5; I
Pred. No. 1.6e-9
43; Mismatches
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Last annotation updat
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Best Local Similarity
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Submitted (APR-2001) t
Submitted (APR-2001) t
EMBL; BC006929; AAH069
EMBL; BC006929; AAH069
01-MAY-1999
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01-DEC-2001
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Q1-DEC-2001 (TrEMBLrel. 19,
Q1-DEC-2001 (TrEMBLrel. 19,
Q1-DEC-2001 (TrEMBLrel. 19,
TRAF-INTERACTING PROTEIN.
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Mammalia; Eutheria;
NCBI_TaxID=10090;
                           Q9YGN2;
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Rodentia;
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91.3%;
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Pred. No. 1.2e
8; Mismatches
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Sciurognathi;
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No. 1.2e-44;
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GH03577P.
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Drosophila m
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                                                                                                                                      RTGFDGLGGRTKFIQPTDTVMIRPLPVKPK
                                                                                                                                                                        KKICKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRSESSCSKDVV
                                                                                                                                                                                           PQNSRVSKASCLHPPSGNEDIDLNMTYDVTTP
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197; Conserv
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Metazoa; Arthropoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                    38.8%;
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                                     19,
19,
19,
                                                                                                                                                                                                                                                                                                                                                                                                            76;
                                    Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                          Score 925; DB 13;
Pred. No. 9.8e-43;
/6; Mismatches 121
                                                                                                                                                       -DSVVILLRTKYKNLVSNQGK
                                                                        PRT;
           fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A8C31AAA4216E8C2 CRC64;
Tracheata;
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  Hexapoda;
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                                     update)
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  Insecta;
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Best Local Similarity 25.1
Matches 113; Conservative
                                                                                                                                                             Q9V8D7;
01-MAY-2000
01-MAY-2000
01-DEC-2001
CG5140 PROTE
MEDLINE-20196006; PubMed-10731132; Adams M.D., Celniker S.E., Holt R.A., Ev Amanatides P.G., Scherer S.E., Li P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Y, CN BW SP;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Chawez C., Dorsett V., Farfan D., Frise E., George R.
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan
Yu C., Lewis S.E., Rubin G.M., Celniker S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY066010; AAL28158.1;
SEQUENCE 435 AA; 48455 MW; OBFFOAC81DD9416E CRC64;
                                        STRAIN-BERKELEY;
                                                                                             Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                    CG5140
                                                                                                                                                                                                                                 Q9V8D7
                                                     SEQUENCE FROM N.A.
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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                       KSH-SPIQDVPKKICKGPRKESQLSLGGQSCAG---
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                                                                                                                                                                                                                                  PRELIMINARY;
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Last sequence update)
Last annotation updat
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Pred. No. 1.6e-08;
2; Mismatches 161;
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  Hoskins
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R.F.,
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RA Ballew R.M. Basu A. Daxendale J. Bayraktaroglu L. Beasley E.M.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Botshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I. Dietz S.M.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I. Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Marvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulip D., Liai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Walson K.A., Nixon K., Nuzskern D.R., Pacleb J.M.,
RA Melson D.R., Welson K.A., Nixon K., Nuzskern D.R., Pacleb J.M.,
RA Melson D.R., Welson K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Welson D.R., Welson K., Weinsenbach J.,
RA Weinson D.R., Weinsers B.D.C., Scheeler F., Shen H.,
RA Weinson D.R., Weinsers B., Weinsenbach J.,
RA Weinson C., Stapheton M., Stupski M.P., Smith T.,
RA Weinson S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Weinson S.M., Woodage T., Weinsenbach J.,
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RA Weinson S.
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                                                            LTMLQETLNLPPVASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPS
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                                                                                                                                FIIDMCSFDCSKLEERVSHLESDLYQAQEKLQAFENKTAYLDSPNASCGLNSNILALKRE
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ERRTTISPTVKENIKR-IEESTSPY-LNIK-
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01-0CT-2000 (T)
01-DEC-2001 (T)
PUTATIVE RING
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Q9M143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lamar B., Stoneking Mayer K.F.X.; Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SEQUENCE
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                                                RDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQDVPKKICKGPRKE------
                                                                                                 MSSFRMLSSDNK - -
                                                                                                                                                KSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRLVLESPAPVEVNLKLRRPSF
                                                                                                                                                                                                 ARSSEKLEKALEKIEKLKKRMRELELITEERENRALRDINVSK---KCSYTEVSEPAIES
                                                                                                                                                                                                                                             S-AVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVYSELDQAKLEL
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                                                                                                                                                                                                                                                                                                                                              KYLEQQQDETKQAQE--EAGRLRSKMKTMEQIELLLQS-----QLPEVEEMIRDMGVGQ
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VSRTDSVIDVDDDYVPETNTSGIRDWNTNIEEKGDNSMVKDIKFNIRKDPTSSVSPYSNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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(TrEMBLrel. 19, Last annotation of the control of the co
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21.5%;
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the EMBL/GenBank/DDBJ databases
c 1 RING-TYPE ZINC FINGER.
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Pred. No. 0.00096;
8; Mismatches 189
                                                                                                 VEKISTPPGKLEEKDGFTIQGSC-----LRGREDSF
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SEQUENCE
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MEDLINE-97442456; Pubmed-9295333;

MISUMI Y., Sohda M., Yano A., Fujiwara T., Ikehara Y.;

Misumi Y., Sohda M., Yano A., Fujiwara T., Ikehara Y.;

"Molecular Characterization of GCP170, a 170-kDa Protein Associated with the Cytoplasmic Face of the Golgi Membrane.";

J. Biol. Chem. 272:23851-23858(1997).

EMBL; D63997; BAA23661.7.;

EMBL; BAA23661.7.;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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VVDVFL
                                                KLDTFL
                                                                                             RPTETQSEQ---
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                                                                                                                                                                                                                                   CKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAIL-----
                                                                                                                                                                                                                                                                                                                           LKLRRPSFRDDIDLNATFDVDTP-----PARPSSSQHGYYEKLCLEKSHSPIQDVPKKI
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                                                                                                                                      PRSESSCSKDVVRTGFDGLGGRTKFTQPTDTVMIRPLPVKPKTKVKQRVRVKTVPSLFQA
                                                                                                                                                                                                                                                                                    LDLRRG---QDEKGAESAGQLFQPCHAHQDPGLPSSRL----
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03; Conservative
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Pred. No. 0.025;
7; Mismatches 194
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RESULT 12
P90990
ID P90990
AC P90990
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Q9DGD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000048; 1
InterPro; IPR001609; n
InterPro; IPR004009; N
InterPro; IPR002928; N
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01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                    1195
                                                                                                                                                                                                                                                                                                                                     1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
SMART; SM00015; IQ; 1.
SMART; SM000242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
                                                                             1419
                                                                                                                             1364
                                                                                                                                                                                1308
                                                                                                                                                                                                                                   1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yoon S., Kakinuma M., Hirayama Y., Yamamoto J., Watabe S.; "cDNA cloning and characterizaion of the complete primary str myosin heavy chain from white croaker fast skeletal muscle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pfam; PF00612; IQ; 1.

Pfam; PF00063; myosin_head; 1.

Pfam; PF02736; myosin_N; 1.

Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB039672; BAB12571.1; -. HSSP; P13538; 2MYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Actanthomorpha; Acanthopterygii; Percomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel.
MYOSIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9DGD5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=118565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sciaenidae;
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                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                           136
                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                             31 LQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREF------
                                                                                                    ETVDRLV-LESPAPVEVNLKLRRPSF
                                                                                                                            AQWRSKYETDAIQRTEELEEAKKKL--AQR-LQDAEEQIEAVNSKCASLEKTKQ--RLQS
                                                                                                                                                                                                                                                                                   VAELGEQIDNLQRVKQKLEKEKSEYKMEIDDLSSNME-----AVAKAKGNLEKMCRTL
                                                                             EVEDLMIDVERANGLAANLDKKORNF
                                                                                                                                                     FSSRSKLQT-----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVAS
                                                                                                                                                                                EELKR----QIEEEVKAKNALAHGVQSARHDCDLLREQFEEEQEAKAELQRGMSKANSEV
                                                                                                                                                                                                      ELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDL
                                                                                                                                                                                                                                EDQLSELKTKNDENVRQINDMSGQRARLLTENGEFTRQVEEKEALVSQLTRGKQAFTQQI 1307
                                                                                                                                                                                                                                                         KKQMKYLEQQQDE-
                                                                                                                                                                                                                                                                                                           ---LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTL 135
                                                                                                                                                                                                                                                                                                                                     LEEISERLEEAGGATASQIEMNKKREAEFQKLRRDL---
                                                                                                                                                                                                                                                                                                                                                                                     ch 7.8%; l Similarity 23.3%; 76; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myosin_tail.
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19,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW.
                                                                                                                                                                                                                                                                                                                                                                                     Score 185.5;
Pred. No. 0.04
63; Mismatches
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Last sequence up
Last annotation
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7.043;
                                                                                                                                                                                                                                                        TKQAQEEAGRL----RSKMKTMEQI
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Euteleostei;
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Neoteleostei
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P90990;

PRELIMINARY;

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Best Local S
Matches 65
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EMBL; U80836; AAB37893.1; -.
InterPro; IPR001841; Znf_ring.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184: PTNC. ?
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Metazoa; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du L., Burton R., Faylon A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Mifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Henkhaus J., Wohldmann P.; "The sequence of C. elegans Submitted (JAN-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
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01-MAY-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                Zinc-finger
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   398
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                                                                                                                                                                                                                                    188
                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                 .2 Mb of contiguous nucleotide
                                                                                                                                        TVVSLQQAL----GKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRSKMKTMEQIELL
                                                                                                                                                                                        FFDL-----AQEEENVLDREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNA
                                                                                                                                                                          FFDVQRMGGEAEKPPEIDYRE-----EHYKLSTSLKVEQEK-----LGTLNTENKNLKD
                                                                                                                                                                                                                                  LQGSCSICFEDLKQNDKISAIVCGHIYHHGCISQWIAT - - KRQCPSCRRTVPKNGFVEKL
                           DLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIMSLKK
                                                                                    LQSQLPEVEEMIRDMGVGQSAVEQLAVYC-----VSLKKEYENLKEARKASGEVADKLRK
                                                                                                                 TVKSLEKKIIREKDKYRQEIPKLQATINHLTISSEETAYLKRELQESKNRLKTCEFYKIL
                                                                                                                                                                                                                                                                                             65; Conserv
                                                                                                                                                                                                                                                                                                                                                                 425 AA; 48104 MW;
                                                                                                                                                                                                                                                                                             Conservative
AAKEIEQLKMEVQS----LKRAAQEDAAIKK
                                                                                                                                                                                                                                                                                                        7.6%;
                                                       -SSEADKQLGEYLKKNGNLDTEKFFQLMKSTNK---
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19,
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Last seq
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EMBL/GenBank/DDBJ
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Pred. No. 0.013;
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                                                                                                                                                                                                                                                                                            102;
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                                                                                                                                                                                                                                                                                                                       Length 425
 424
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RESULT Q9AV25

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RESULT 042352

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
1239
                                                                                                                                                                                           1063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 CTICSDFFDHSRDVAAI-----HCGHTFHLQCLIQSFETAPSRTCPQCRIQVGKRTII
                                                                                                                                                                                                                                                                                                                                                                                                                                              QVEAQKVELKLQMDESRSLITNLKDELEQVEAQKVELKLQMDESRSLITNLKDELEQVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NKLFFDLAQEEENVLDREFLKNELDNVRAQLSQKDKEKR-----DSQVIIDTLRDTLE
                                                                                                                                                                                         SILRADKAKLEANLEDVNAQMIHYESQLEDLRESKTKIKDLVDSLNASKQNEEMLTTDVD
                                                                                                                                                                                                                                                                                                                     VHGYASHLEQELEQSKRKTMDFCKTLESLEAKLSSLQEDISLKEQSLLSELENIFQEHKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKL-----EHENVELSEF----ISGLESQLTYLANEKELSMLQMDESRSLITNLKDELE
EISAQTKLVMLGD----
                             -LGGRTKFIQPTDTVMIRPLPVKPKTKV
                                                                                           EELVGAFPI - - - - FVRNAILGQKQPKRPRSES
                                                                                                                                                         T-----PPARPSSSQHGYYEKLCLEKSHSPIQDVPKKICKGPRKESQLSLGGQSCAGEPD
                                                                                                                                                                                                                       RLVLESPAPVEVNLK----
                                                                                                                                                                                                                                                      HEERIDRVHLLLNKIEKEKTVELSNLEREVISLTAQLSSTEEERE-----SSTLDTIREV
                                                                                                                                                                                                                                                                                      ----LDQAKLELKSAQK----DLQSADKEIMSLKKKLTMLQETLNLPPVASETVD----
                                                                                                                                                                                                                                                                                                                                                    SGEVADKLRKDLFSSR----
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                                                           EVLTLQSSLDEAKFEKGKLEGLIQSLSEECEELKAQKGMLTDKVSCMQDTLNAANEGKQI
                                                                                                                          NMRRSIEAAR--SNEDNLRKTLCELELKSKSSDYEKQ--QIIEEISVLKIQVHKIAGLQD
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21.7%;
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yta; Liliopsida;
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a; Poales; Poaceae;
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                                                                                           SCSKDVVRTGFDG---
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Best Local S
Matches 92
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InterPro; IPRO1609; Myosin_N.
InterPro; IPRO14009; Myosin_Lail.
Pfam; PF00612; IQ; 2.
Pfam; PF00063; Myosin_head; 1.
Pfam; PF00736; Myosin_head; 1.
Pfam; PF001736; Myosin_heal; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000335; Myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
SMART; SM00242; MYSC; 1.
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Cyprinus carplo (Common carp).

Eukaryota; Metazoa; Chordata; Craniata;

Actinopterygii; Neopterygii; Teleostei;

Cypriniformes; Cyprinidae; Cyprinus.
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01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                     1484
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MEDLINE=97352533; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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EAESTLEHEESKI 1556
                        GOSCAGEPDEELV
                                                                                                                                    DRLV-LESPAPVEVNLKLRRPSFRDDI----
                                                                                                                                                                                      RSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETV
                                                                                                                                                                                                                                                                                      VAELGEQIDNLQRVKQKLEKEKSEYKMEIDDLTSNME-----AVAKAKGNLEKMCRTL
                                                                                                                                                                                                                                                                                                                                                                                   LEEISERLEEAGGATAAQIEMNKKREADFQKMRRDL---EESTLQHEATAAALRKKQADT
                                                                                                                                                                                                                                                                                                                                                                                                            LQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREF-------
                                                  NSYEEALDHLETLKRENKNLQQEISDLSEQLGETGKSIHELEKAKKIVESEKAEIQTALE
                                                                             HGYYEKL----CLEKSHSPIQ------
                                                                                                        DLMIDGERANALAANLDKKQRNF-DKVLAEWKQKYEESQAELEAAQKEARSLSTELFKMK
                                                                                                                                                               RAKYETDAIQRTEELEEAKKKL--AQR-LQDAEESIEAVSSKCASLEKTKQ--RLQGEVE
                                                                                                                                                                                                                 IEDLQRHVEEEVKAKNALAHAVQSARHDCDLLREQYEEEQEAKTELQRGMSKANSEVAQW
                                                                                                                                                                                                                                            -----EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSS
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D89991; BAA22068.1;
P13538; 2MYS.
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21.2%; Pred. No. 0.075;
Live 80; Mismatches 163;
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05, Last sequence update)
19, Last annotation update)
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Euteleostei;
                                                                                                                                  -DLNATFDVDTPPARPSSSQ-----
                                                                            -----DVPKKICKGPRKESQLSLG
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Best Local :
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Pfam; PF00063; myosin_N; 1.
Pfam; PF02736; Myosin_Tail; 1.
Pfam; PF01576; Myosin_Tail; 1.
PF10157; PR00193; MYOSINHEAVY.
PRINTS; PR00194; TROPOMYOSIN.
ProDom; PD000355; myosin_head; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification of two distinct muscles in the planarian, | japonica, by the expression of myosin heavy chain genes."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AB015484; BAA34954.1; -
HSSP; P24733; IWDC. Interpro; IPR001637; GlnA_adenv1+~
Interpro; IPR001637; GlnA_adenv1+~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001609; InterPro; IPR004009; InterPro; IPR002928; InterPro; IPR002933;
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01-MAY-1999
01-MAY-1999
01-DEC-2001
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SMART; SM00242; MYSC; 1.

PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.

PROSITE; PS00182; GLNA_ADENYLATION; UNKNOWN_1.

PROSITE; PS50096; IQ; 1.

SEQUENCE 1958 AA; 224857 MW; 3FE254327DF89524
1168 KR
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Paludicola; Dugesiidae;
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Eukaryota; Metazoa; Platyhelminthes;
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                                                                                                                                              LTMLQETL --
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                                                                                               IQELEEDLEAERQARAKAEKSRHQLEGELEELSDRLEEQGGATSAQLELNKKREAELLKL
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Myosin_tail
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Last annotation updat
                                                                                                                                              NLPPVASETVDRLVLE---SPAPVEVN-----LKL
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Pred. No. 0.
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Q90338;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1998 (TrEMBLrel. 05, Last sequence)
Q1-JAN-1998 (TrEMBLrel. 19, Last annotation)
MYOSIN HEAVY CHAIN (FRAGMENT).
Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Actinopterygii; Neopterygii; Teleostei; Eu
                                                                                                                                 Q9Y577
Q9Y577;
01-NOV-1999
01-NOV-1999
01-DEC-2001
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TISSUE-FAST MUSCLE;
MEDLINE-97176447; PubMed-9023993;
Imai J., Hirayama Y., Kikuchi K., Kakinuma
"CDNA cloning of myosin heavy chain isoform
muscle and their gene expression associated
SEQUENCE FROM N.A.
TISSUE-TESTIS;
MEDLINE-99011410; PubMed-9792805;
Ogawa S., Goto W., Orimo A., Hoso
Inoue S.;
                                                                                                                      RING
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SEQUENCE
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J. Exp. Biol. 200:27-34(1997).
EMBL; D50475; BAA09068.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002928; Myosin_tail.
InterPro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
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                                                                      NCBI_TaxID=9606;
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OV-1999 (TrEMBLrel. 12,
EC-2001 (TrEMBLrel. 19,
FINGER PROTEIN TERF.
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                                                                                                                                                                                  PRELIMINARY;
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                                                                                   Chordata;
Primates;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 180; DB 1
Pred. No. 0.046;
7; Mismatches 1
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                                                                                Craniata; V
Catarrhini;
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Euteleostei;
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; Ostariophysi;
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InterPro; JPR001870; Gamma_carbxylse.

InterPro; JPR003877; SPRY.

InterPro; JPR003877; SPRY.

InterPro; JPR003878; SPRY_domain.

InterPro; JPR00315; Znf_bbox.

InterPro; JPR001841; Znf_ring.
                                                                                             Q22276 PRELIMINARY;
Q22276; Q22294;
Q1-NOV-1996 (TIEMBLICE). 0
01-MAY-1999 (TIEMBLICE). 1
01-MAY-2000 (TIEMBLICE). 1
                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogawa S., Inoue S.;
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pfam; PF00643; zf-B_box; 1.

pfam; PF00097; zf-C3HC4; 1.

PRINTS; PR01406; BBOXZNFINGER
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SEQUENCE
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$M00184; RING; 1.
$M00449; $PRY; 1.
E; P$00518; ZINC_FINGER_C3HC4;
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                                          Nematoda; Chromadorea; cinae; Caenorhabditis.
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Pred. No. 0.02
56; Mismatches
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Best Loc
Matches
                                          EMBL; $78540; AAB34772.2; InterPro; IPR002928; Myosin_tail. InterPro; IPR00533; Tropomyosin.pfam; PF01576; Myosin_tail; 1. PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                       AMHC1.
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q91411 PRELIMINARY; PRT; 764 AA.
Q91411;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN HEAVY CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                 TISSUE-HEART ATRIUM;
MEDLINE-95324374; PubMed-7600964;
Yutzey K.E., Rhee J.T., Bader D.;
"Expression of the atrial-specific
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EMBL; Z48055; CAA88136.1; -.
EMBL; Z29443; CAA88136.1; -.
EMBL; Z29443; CAA82580.1; -.
EMBL; Z48055; CAA82580.1; JOINED.
SEQUENCE 1138 AA; 132785 MW;
                            NON_TER
                                                                                                                                                                             Development 120:871-883(1994).
                                                                                                                                                                                                          heart.";
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     764 AA;
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     88869 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65;
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Pred. No. 0.05
65; Mismatches
  35AC9C64967FD1C2 CRC64;
                                                                                                                                                                                                                            ic myosin polarity
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                                                                                                                                                                                                                            heavy chain AMHC1 in the developing
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Best Local
                                   InterPro; IPR003878; SPRY_dom
InterPro; IPR000315; Znf_bbox
InterPro; IPR001841; Znf_ring
Pfam; PF00622; SPRY; 1.
Pfam; PF00643; Zf-B_box; 1.
Pfam; PF00097; Zf-C3HC4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=TESTIS;
MEDLINE=99011410; Pu
Ogawa S., Goto W., (
                                                                                                                                                                                                                    Submitted (JUN-1999) to the EMBL/GenE-!- SIMILARITY: CONTAINS 1 RING-TYPE EMBL; AF156272; AAD40287.1; -HSSP; P15919; 1RMD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9WV59;
                                                                                                                                                                                                                                                                                                               Ogawa S., Goto W., Orimo Inoue S.;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, RING FINGER PROTEIN TERF.
                                                                                                                                                                                                                                                                                                                                                                                                                           protein, terf, expressed in the testis.";
Biochem. Biophys. Res. Commun. 251:515-519(1998
                     PRINTS;
                                                                                                                                                                            InterPro;
                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of a novel RING finger-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inoue S.;
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SM00336;
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                                                                                                                                                                            IPR001870; Gamma_carbxylse
IPR003877; SPRY.
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                       BBOXZNFINGER
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Orimo A., Hosoi
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23.1%;
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                                                                                                         Znf_ring
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Last
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                                                                                                                                                                                                                                                                                                                                       Hosoi T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                             Q9UIK7
Q9UIK7;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
                                                                                                                                                                                    "Fusion of a Novel Gene, ELKS, to c-ret in a Farcinoma.";

Carcinoma.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ EMBL; AB015617; BAA88763.1; -

InterPro; IPR002017; Spectrin.

SEQUENCE 948 AA; 108792 MW; 344297FDFC9F7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00184; RING; 1.
SMART; SM00449; SPRY; 1.
PROSITE; PS00518; ZINC_FINGER_C3HC4;
Zinc-finger_
                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                  Nakata T.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                           511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 KRTI; INKLF---FDLAQEEENVLDREFLKNELDNVRAQLSQKDKE---KRDSQVIIDTL
                                                   60
                                                                                                   œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 ALCTICSDFFDHSRDVAAIHCGHTFHLQCLIQSFETAPSR-----TCPQCRIQVG
                                                                                                  TICSDFFDHSRDVAAIHCGHTFHLQCLIQSFETAPSRTCPQCRIQVG -----KRTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVAIKTVCRV----PGQIEV-LK----SFQEDV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVASETVDRLVLESPAPVEVNLKLRRPSFRDDI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYL--EQQQDETKQAQEEAGRLRSKMKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRNLRP\RLLTKVAEMARQHPGLHKRDL------CQIHQEPLKLFCQDDQTPICVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCSICLDYF - - - TDPVMTACGHNFCRECIQMSWEKGKGKKKGKKKQKGSFPCPECREMSP
VIIDTLRDTLEERNATVVSLQQALGKAEMLCSTLKKQMKYLEQQQDETKQAQEEAGRLRS
                        NKKTKQIQDMAEEKGTQAGEIHDLKDMLDVKERKVNVLQKKIENLQEQLRDKEKQMSSLK
                                        N---KLFFDLAQEE------ENVLDRE-----FLKNELDNVRAQLSQKDKEKRDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GK-LQDSKASLDHQSRSLDLILLQLEEQTQQEPLQMLQDVKDTLTRKESLSMQYPEVVL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKDLFSSRSKLQTVYSELDQAKLEL--KSAQKDLQSAD--KEIMSLKKKLTMLQETLNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KERRERILE----EFQKVVLFL-----VEEERRLLQILKKEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REAQEHRMHRVLPLDEAAREYKL----RLEEDIKYLREEMMKTETLQAKEEQTLTEWQERV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 AA; 54954 MW;
                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                        7.4%;
20.3%;
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                                                                                                                            80;
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                                                                         -HIEVLKESL-TAKEQRAAILQTEVDALRLRLEEKETML
                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                      Score 177.5; DB Pred. No. 0.054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.01
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 178;
                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1AAB42BB02615ADF
                                                                                                                           Mismatches 135;
                                                                                                                                                                                        344297FDFC9F7602
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                                                                                                                                                                                                                                                                                                                   Hominidae;
                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114;
                                                                                                                                                                                                                                                     Papillary Thyroid
                                                                                                                                                                                                                            databases
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                                                                                                                                                  Length
                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                           111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72;
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
  161
                                                101
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                        570
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                             Lightning J.;
Submitted (JUN-1994) to the EMBL/G
EMBL; Z34801; CAA84332.1; -.
EMBL; Z366514; CAA84332.1; JOINED.
EMBL; Z36514; CAA91344.1; -.
EMBL; Z34801; CAA91344.1; JOINED.
InterPro, IPR000237; GRIP.
Pfam; PF01465; GRIP. 1.
SEQUENCE 1133 AA; 129239 MW; 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q21022; Q21071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q21022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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                         284
                                                    288
                                                                                                                                                                                                                                                                                                                   Local Local 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 LVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEK
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                                                                                                                                                             VSKKLDSSETSLKEFSDMIEAMKIQLINCEKQKDEAVELLKQ-KLEEVEKNMSDVEVQKQ
                                                                                                                                                                                                                                                                                                  CPQCRIQVGK----RTIINKLFFDLAQEEENV------LDREFLKNELDNVRAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNDKDKKIAELESLTSRQVKDQNKKVANLKHKEQVEKKKSAQMLEEARRREDNLNDSSQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MESQLKKAHEAALEAR-ASPEMSDRIQHLEREITRYKDESSKAQAEVDRLLEILKEVENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLKDLKEKVSLLQGDLSEKEASLLDLKEHASSLASSGLKKDSRLKTLEIALEQKKEECLK 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERVKSLQADTTNTDTALTTLEEALAEKERTIERLK-----EQRDRDEREKQEEIDNYKK
                                                                                                                                                                                       LEQQQDETKQAQEEAGRLRSKMKTM------EQIELLLQSQLPEVEEMIRDMGVGQ-
                                                                                                                                                                                                                   QLAKAMEKLNSEQNILDEVTKKLEQSEEEVLAARGAIQELTEKLEESEKETSTAKTELEA
                                                                                                                                                                                                                                             LSQKDKEKRDS-QVIIDTLRDTLEERNATVVS-----LQQALGKAEMLCSTLKKQMKY
                                                                                                                                                                                                                                                                        CDALQAEVNEAKALREEIQAKYDDVTQKAERIQGELEESKKVLESEKQAFENEKEQEREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQSADKEIMSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KMKTMEQIELLLQSQLPEVEEMIRDMGVGQS-------AVEQLAVYCV-
                        ASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLE
                                                   SSAISEITKQMEAAKKELEASEKEKSELREQMDRLQKVHNAGQEDIQKLQKTWELEMAKI
                                                                                                         LLLESTTSEMKQHAEAAEIVKKQ---LEEAQSS----IENLKKDAENERN-LKTALESDE
                                                                              -SELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQET----
                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                           SAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVY----
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          7.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                103;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.066;
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                                                                                                                                                                                                                                                                                                                              169;
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                                                                                                                                                                                                                                                                                                                              Indels 123;
                                                                                                                                                                                                                                                                                                                                                       Length 1133;
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                                                                              LNLPPV
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348

AKSTEDE --

KLAREQLAGELE - NAKEDL - - -

KVVEE

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RESULT

Q9FJ35

ID Q9

AC Q9

DT Q1

DT Q1

DT Q1

DT Q1

DT Q1

DT Q1

RC SE

OC SE

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Q9FJ35;
Q9FJ35;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN HEAVY CHAIN-LIKE PROTEIN.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; core eudicotyledons; Spermatophyta; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                1061
        1239
                                                                                                             1181
                                                                                                                                                                                                                        1121
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DNA Res. 5:297-308(1998).
EMBL; AB016871; BAB10654.1; -.
SEQUENCE 1305 AA; 149961 MW; F37284B8E7BBF217 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           1016
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MEDLINE-99087489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakamura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                     227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167
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                                                                                                                                                                                                               LSNQKLRVTEQVLTEKEEAFRKEEAKHLEEQALLEKNLTMTHETYRGMIKEIADKVNITV
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                                                                                                          DGFQSMSEKLTEKQGRYEKTVMEASKILWTATNWVIERNHEKEKMNKEIEK--
                                                                                                                                      DVDTPPARPSSSQHGYYEKLCLEKS---
                                                                                                                                                                                                                                                                        SLKKKLTMLQETLNLPPVASETVDRLVLESPAPVEVNLKLRPSFRDDI-----DLNATF
                                                                                                                                                                                                                                                                                                                             VDYKEAQRLLEERGKEVTSRDSTIGVHEETMESLRNELEMKGDEIETLMEKISNIEVKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEETINKV-----KVHESILEEINGLSEKIKGRELELETLGKQRSELDEELRTKKEENVQ
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                                                  LGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRSESSCSKDVVRTGFDGLGGRTKFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                     -LSNQITDVQKAL------VEQEAAY-NTLEEEHKQINELFKETEATLNKVT
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S., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.4%;
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-MKETLMGLGEEKREAIRQLC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 177.5; DB 10;
Pred. No. 0.076;
Pred. No. 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaneko T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Embryophyta; Tracheophyta; edons; core eudicots; Rosic
                                                                                                                                                             HSPIQDVPKKICKGPRKESQLS
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  -VWIDHHRSRCEYL
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Best Local S
Matches 74
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J. Exp. Biol. 200:27-34(199
EMBL; D89990; BAA22067.1; -
EMBL; D50474; BAA09067.1; -
HSSP; P13538; 2MYS.
                                                                                                                                                                                                                                             1142
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                                               1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Myosin.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS: PR00193; MYOSINHEAVY.
PRODOMS: PD000355; myosin_head;
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hirayama Y., Watabe S.;
"Structural differences in the crossbridge head of
associated myosin subfragment-l isoforms from carp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-FAST SKELETAL MUSCLE;
MEDLINE-97352533; PubMed-9208928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostel;
Cyprihiformes; Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrembLrel. 01, 01-NOV-1998 (TrembLrel. 08, 01-DEC-2001 (TrembLrel. 19, MYOSIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00015; IQ; 1
SMART; SM00242; MYSC;
PROSITE; PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
Pfam; PF07736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             muscle and their gene expression associated with temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97176447; PubMed=9023993;
Imai J., Hirayama Y., Kikuchi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=FAST SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                muscle."
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    179
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                                                                                                                                                                                           79
                                                                                                                                                                                                                                                                                          31 LQCLIQSFETAPSRTCPQCRIQVGKRTIINKLFFDLAQEEENVLDREF----
                                            EDQLSEIKAKSDENSRQLNDMNAQRARLQTENGEFSRQLEEKEALV-SQLTRGKQAFTQQ
                                                                                            KKQMKYLEQQQDETKQAQEEAGRLRSKMKT---
                                                                                                                                              VAELGEQIDNLQRIKQKLEKEKSEYKMEIDDLSSNME-----AVAKAKGNLEKMCRTL
                                                                                                                                                                                                                                          LEEISERLEEAGGATAAQIEMNKKREAEFQKMRRDL---EESTLQHEATAAALRKKQADS
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                                                                                                                                                                                           --- LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTL
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74; Conserv
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EVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yama Y., Kikuchi K., Kakinuma M. of myosin heavy chain isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200:27-34(1997).
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                                                                                         --MEQIELLLQSQLP----
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Best Local S
Matches 107
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Hu H., Merrifield P., Atkinson B.G.;
"Expression of the Myosin Heavy Chain Gen
Thyroid Hormone-induced Metamorphosing Ra
Dev. Genet. 0:0-0(1999).
EMBL; AF097904; AAD13769.1; -.
Interpro; IPR002928; Myosin_tail.
Interpro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00194; TROPOMYOSIN.
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Q9YHD8;
Q9YHD8;
01-MAY-1999
01-MAY-1999
01-JUN-2001
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Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1426
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EGDLNELETQLSHANRQAAEAQKQLRNVQAHLKDNQLQLDD---ALRSQEDLKEQVAVVE
                                                                                                                                                              LNLPPVASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVD----TPPARPSSSQ
                                                                                                                                                                                                                     KNLQQEISDLTEQISETGKTVHELEKAKKLVEQEKSDLQAALEEAEGSLEHEESKILRIQ
                                                                                                                                                                                                                                                                                                                            DKKQRNFDKVLAEWKQKYEEAQAELESALKDARSMSTEIFKMKNAYEESLDQLETLKREN
                                                                                                                                                                                                                                                                                                                                                                                                                                               AKKKLAQRLQE---AEEQVEAVNSKCASLEKTKQRLQA---EVEDLMVDVERSNSAAAAL
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                                                   HGYYEKLCLEKSHSPIQ--DVPKKI---CKGPRKESQLSLGGQSCAGEPDEELVGAFPIFV
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107; Conservative
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(TrEMBLrel. 10, Last sequence up
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                                                                                                                                                                                                                                                                           -KDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEIM-SLK-KKLTMLQET
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Pred. No. 0.053;
82; Mismatches 184;
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01-JAN-1998
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SEQUENCE FROM N.A.
Monier S., Janoueix-Lerosey
Monier S., Janoueix-Lerosey
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028714;
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EMBL; AF340028; AAX56381.1; -.
InterPro; IPR002017; Spectrin.
InterPro; IPR000533; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
SEQUENCE 976 AA; 111931 MW; 4
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Mammalia; Eutheria;
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14;

CHROMOSOME SEGREGATION

PROTEIN (SMC1)

AF1558

Archaeoglobus fulgidus

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Best Loc
Matches
                                                  066878 PRELIMINARY;
066878;
01-AUG-1998 (TrEMBLrel. 07,
01-BUG-2001 (TrEMBLrel. 19,
                  CHROMOSOME ASSEMBLY XCPC OR AQ_629.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003439; ABC_transportr.
InterPro; IPR003405; SMC_N.
InterPro; IPR003395; SMC_N.
InterPro; IPR002017; Spectrin.
Pfam; PF02483; SMC_C; 1.
Pfam; PF02463; SMC_N; 1.
Pfam; PF02463; SMC_N; 1.
PFOSTTE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
UNDERPORTER; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Complete proteome SEQUENCE 1156 AA; 134244 MW; 18CB16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
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MEDLINE=98049343; I
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Archaeoglobus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complete genome sequence of the hyperthermophilic,
                                                                                                                                                                                                                                                  RRPSFRDDIDLNATFDVDTPPARPSSSQHGYYEKLCLEKSHSPIQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                 STFGDVNLKAIQEYEEVKARRDELVE --- KKMVLEKERADILD
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PubMed=9389475;
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21.48;
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                                    Last sec
Last anr
HOMOLOG.
                                                                                       Created)
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Best Local S
Matches 86
                                                                                                    O9TV61;
O1-MAY-2000 (TrEMBLrel.
O1-MAY-2000 (TrEMBLrel.
O1-DEC-2001 (TrEMBLrel.
MYOSIN HEAVY CHAIN 2X.
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InterPro;
                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                       Sus scrofa (Pig).
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InterPro;
 SEQUENCE
                                NCBI_TaxID=9823;
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EMBL; AE000699; AAC06839.
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NCBI_TaxID-63363;
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arPro; IPR003487; ATP_GTP_A.
erPro; IPR003716; RNA_pol_omega.
erPro; IPR003405; SMC_C.
erPro; IPR003395; SMC_N.
erPro; IPR003395; SMC_N.
erPro; IPR002317; Spectrin.
n; PF02483; SMC_N; 1.
SITE; PS00211; ABC_TRANSPORTER; UNIVERSITE; PS00211; ABC_TRANSPORTER; UNIVERSITER; UNIVERSITER; PS00211; ABC_TRANSPORTER; P
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l Similarity 22.0%;
86; Conservative 8
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                                                 Chordata; Crania:
Cetartiodactyla;
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19,
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Last sequence
Last annotation
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Pred. No. 0.08
98; Mismatches
                                                    Craniata; Ver
actyla; Suina;
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annotation
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                                                    Vertebrata;
ina; Suidae;
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081;
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Euteleostomi; Sus.

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Deckert G., Warren P.V., Gaasterland T., Young W.G., Le
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                          of the hyperthermophilic bacterium Aquifex
B12DB30F70C0CE49
CRC64;
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Length 1156;

232 LLKEKEKLLKERERILNELSSLRESLEDITFQIQENEKELNERERLLKEVNEKIMPFKEK 291 66 LAQEEENVL-DREFLKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQA 124 LEREVGTLQLELEK-----LKEEYKSLKEVER-----EKLR-ELEEEEERLKITFDE DVSDVFKDIKGVYGSVSELIRVKNPEHITAIEVAG----GGRLKFIVVEDEEVAKECIQLA EKEQEIK-RIKAIKKKEEEEIRNLTQELNIYEKRLSEVRKKLEEVLKEKGAIEREVRSFS MIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTVYSE LGK--AEMICSTIKKQMKYLEQQQDETKQAQEEAGRIRSKMKTMEQIELLLQSQLPEVEE PAPVEVNLKLRRPSFRDDIDL-NATFDVDTPPARPS----SSQHGYYEKLCLE---KSHS VKKLEEEKKLTEKLNSLNKEKQELEIQRANLKNKIERIKEDIN--KLISEREEKIKEIK L-----DQAKL--ELKSAQKDLQSADKEIMSLKKKLTMLQETLNLPPVASETVDRLVLES VGKFTAE-----IENAERSIKEKERELKESENRVKNLEE---LINNLLSDKEN -CKGPRKESQLSLGGQSCAGE-----PDEEL----Indels 84; Gaps 556 499 182 347 440 295 382 242 336 381 19;

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Best Local S
Matches 87
                                                     D Q98TQ6 PRELIMINARY; PRT; 1929 AA.
C Q98TQ6;
C Q98TQ6;
T 01-JUN-2001 (TrEMBLrel. 17, Created)
T 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
T 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
E MYOSIN HEAVY CHAIN.
N MYOSIN HEAVY CHAIN.
S Notothenia coriiceps (black rockod).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
C Eukaryota; Metazoa; Chordata; Craniata; Perciformes;
C Actinopterygii; Neopterygii; Percomorpha; Perciformes;
C Nototheniddei; Notothenidae; Notothenia.
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Pfam; PF00613; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY;
ProDom; PD000355; myosin_head; 1
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InterPro; IPR001609; m
InterPro; IPR004009; m
InterPro; IPR002928; h
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Meat Sci. 57:311-317(2001)
EMBL; AB025262; BAA82146.1
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     SEQUENCE FROM N.A
                                    NCBI_TaxID=8208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Myosin_N.
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Pred. No. 0.14
81; Mismatches
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                                                                                                                Euteleostomi;
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01-MAY-2000
01-JUN-2001
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SMART; SN
SEQUENCE
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                     EMBL;
MGD; N
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Gauvry L., Ennion S., Ettelaie C., Goldspink G.;

"Characterisation of red and white muscle myosin heavy coding sequences from Antarctic and tropical fish.";

Comp. Biochem. Physiol. 127:575-588(2000).

EMBL; AJ243767; CAC27776.1; -.

HSSP; P13538; 2MYS.
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; PF00063; myosin_head; 1.
pfam; PF02736; Myosin_N; 1.
pfam; PF01576; Myosin_tall; 1.
pfam; PF01576; MYOSINHEAVY;
pRINTS; PR00193; MYOSINHEAVY;
                            InterPro; IPR001609;
InterPro; IPR004009;
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                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=99303627; PubMed=10373470;
                                                                                                                                                                                                                          Mus musculus (Mouse).
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NON_TER
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                MGI:1915046;
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sm00015; IQ; 1.
sm00242; MYSC; 1.
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Last annotation updat
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Pred. No. 0.
                                                                                                                                                                                      Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310
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044929 OTTEMBLE 06, C.
01-JUN-1998 (TREMBLE 1. 06, L.
01-JUN-2001 (TREMBLE 1. 17, L.
MICROTUBULE BINDING PROTEIN D
CLIP-190 OR CG5020.
                                                                                                                                                                                                                                                                                                              STRAIN-OREGON R;
Lantz V.A., Miller K.G.;
J. Cell Biol. 0:0-0(1998).
EMBL; AF041382; AAB96783.1;
                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                               FlyBase; FBgn0020503; CLIP-190.
InterPo; IPR00938; CAP-GLY.
Pfam; PF01302; CAP-GLY 2.
SEQUENCE 1690 AA; 189103 MW;
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NGSLEEEAKKSGQLQEQITKLKSEVEETQAALSSYHTDVESKTKQLEAANAALEKVNKEY
                       --NLKEARKASGEVAD---KLRKDLFSSRSKLQTVYSELDQAKLELKSAQKDLQSADKEI
                                                QVQLEQLQQQAAASGEEGSKTVAKLHDEISQLKSQAEETQSELKSTESNLEAKSKQLEAA
                                                                      E-QIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYE--
                                                                                                QQQLEEKTLGHEKLQAAL-----EELKKEKETIIKEKEQELQQLQSKSAESESALKVV
                                                                                                                      RDTLEERNATVVSLQQALGKAEMLCSTLKKQMK-YLEQQQDETKQAQEEAGRLRSKMKTM
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; Pred. No. 0.2;
63; Mismatches
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Pred. No. 0.14
84; Mismatches
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Kikuno R., Nagase T., Ishikawa K., Hirosawa M., Miyajima N
Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human
"Precomplete sequences of 100 new cDNA clones from brain w
for large proteins in vitro.";
DNA Res. 6:197-205(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SFRDDIDLNATFDV --
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361
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В Ş В

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RESULT PRESULT PRESULT
RESULT
Q9YHD4
ID Q9
AC Q9
DT 01
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Q9YHD4
Q9YHD4;
01-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN HEAVY CHAIN (FRAGMENT).
Theragra chalcogramma.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Actinopterygii; Perecontali; Gadiformes; Gadoidei; Gadidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002928; Myosin_tail.
InterPro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-FAST MUSCLE;
Togashi M., Hirayama Y., Kakinuma M., Watabe
"cDNA cloning of Alaska polack fast skeletal
chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P13538; 2MYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB000214; BAA19070.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=48550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAELGEQIDNLQRVKQKLEKEKSEFKMEIDDLSSNME-----AVSKAKGNLEKICRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---LKNELDNVRAQLSQKDKEKRDSQVIIDTLRDTLEERNATVVSLQQALGKAEMLCSTL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KETHLT 423
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                                                                                                                                                                   PVASETVDRLV-LESPAPVEVNLKLRRPSF: | | :| :| :| :| :|
                                                                                                                                                                                                                                                                                                                                                                                                                                 KKQMKYLEQQQDETKQAQEEAGRLRSKMKT-----MEQIELLL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEEISERLEEAGGATSAQIEMNKKREAEFQKLRRDL---EESTLQHEATAAALRKKQADS
                                                                                                                                                                                                                                                               RKDLFSSRSKLQT----VYSELDQAKLELKSAQKDLQSADKEIMSLKKKLTMLQETLNLP
                                                                                                                                                                                                                                                                                                            EELKRQNEEEVKAKNALAHGVQSARHDCDLLREQFEEEQEAKAELQRGMSKANGEVA---
                                                                                                                                                                                                                                                                                                                                                  EEMIRDMGVGQSAVEQLA-----VYCVSLKKEYENLKEAR-----KASGEVADKL
                                                                                                                                                                                                                                                                                                                                                                                          EDQLSEIKAKSDENARQVNDISAQRARLLTENGEFGRQLEEKEALVSQLTRGKQAYTQQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Similarity
79; Conserv
                                                                                                                                                                                                                           -QWRSKYETDAIQRTEELEESKKKL--AQR-LQEAEEQIEAVNSKCASLEKTKQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
    (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.3%;
23.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128626 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 174.5; DB Pred. No. 0.094;
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muscle
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RESULT
Q98TQ5
ID Q0
AC Q0
DT 00
DT 00
DT 00
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Best Local
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Q98TQ5;
Q98TQ5;
01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002017; Spectrin.
InterPro; IPR000533; Tropomyosin.
Pfam; Pf01576; Myosin_tail; 1.
PRINTS; PR00194; TROPOMYOSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thyroid Hormone-induced Metamorphosing Dev. Genet. 0:0-0(1999).
EMBL; AF097908; AAD13773.1; -.
InterPro; IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-TAIL MUSCLE, HINDLIMB MUSCLE;
HU H., Merrifield P., Atkinson B.G.;
"Expression of the Myosin Heavy Chain Genes in the Tail Muscle
"Expression of the Myosin Heavy Chain Genes at the Tail Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; V
Amphibia; Batrachia; Anura; Neobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation updat MYOSIN HEAVY CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana catesbeiana (Bull frog).
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                                                                                                                       36
                                                                                                                                                                                                                         KLD
                                                                                                                                                                                    EVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATVVSLQQALGKAEMLCS-------TLKKQMKYLEQQQDETKQAQEEAGRLR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEKESLVSQLSRGKQAFTQQTEELKRQLEEETKAKNALAHALQSARHDCDLLREQYEEEQ
                                                                                                                                                                                                                                                                 ALEQTERGRKVAEHELLDVTERVQLLHTQNTSLI-----NTKKKLEADV---
                                                                                                                                                                                                                                                                                                          ---ESSCSKDVVRTGFDGLGGRTKFIQPTDTVMIRPLPVKPKTKVKQRVRVKTVPSLFQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESGKSIHETEKAKKQVEQEKSELQSALEEAEGSLEHEEAKILRVQLELNQVKSE-VDRKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYEEAQAELEAAQKESRGLSTEVF-KMKNNYEEALDQLETLKRENKNLQQEISDLTEQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KEARKASGEVADKLRKDLFSSRSKLQTV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKCASLEKTKQRLQA---EVEDLMYDVERSNSA-----CTALDKKQKNFYKVLSEWKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKMKTMEQIELLLQSQLPEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENL-----
                                                                                                                                                                                                                                                                                                                                                  RQAAEAQKQLRNVQGQFKDAQLHLDD----AIRGNDDLKEQLAIVERRNNLMQAEIEEMRS
                                                                                                                                                                                                                                                                                                                                                                         IQ--DVPKKI--CKGPRKESQLSLGGQSCAGEPDEELVGAFPIFVRNAILGQKQPKRPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                 AEKDEEIE---QLKRNSQRALESMQTSLDSEVRSRNDALRLKKKMEGDLNEMEIQLSHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LESPAPVEVNLKLRRPSFRDDIDLNATFDVD----TPPARPSSSQHGYYEKLCLEKSHSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAKAELQRSLSKANSEVSQWRTKYETDAIQRTEELEEAKKKLAQRLQE---AEEQIEAVN
                                                                                                                                                                                                                         464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -YSELDQAKLELKSAQKDLQSADKEIM-SLK-KKLTMLQETLNLPPVASETVDRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    671 AA;
(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.3%;
21.9%;
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  17,
17,
19,
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Last sequence up
                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
eobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1904A262790CA26F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 167;
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                     update)
update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        671;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rana.
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Best Local
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                                                                                                                                                                                                                                                                                                      096063;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MYOSIN HEAVY CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gauvry L., Ennion S., Ettelaie C., Goldspink G.;
"Characterisation of red and white muscle myosin heavy
coding sequences from Antarctic and tropical fish.";
Comp. Biochem. Physiol. 127:575-588(2000).
EMBL; AJ243768; CAC27777.1;
-...
HSSP; P03437; 1HTM.
                                                                                                                                                                                                       Dugesia japonica (Planarian).
Eukaryota; Metazoa; Platyhelminthes;
Paludicola; Dugesiidae; Dugesia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR002928; Myosin_tail.
Interpro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00194; TROPOMYOSIN.
NON_TER 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;

Notothenioidei; Nototheniidae; Notothenia.
  SEQUENCE FROM N.A Kobayashi C., Koba
                                                                            SEQUENCE FROM N.A.
Kobatashi C., Agata
Submitted (JUN-1998)
                                                                                                                                                                                NCBI_TaxID=6161;
                                                                                                                                                                                                                                                                                      ДЛМНС-В.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DELKR----QIEEEVKAKNALAHGLQSARHDCDLLREQFEEEQEAKAELQRGMSKANSEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQWRSKYETDAIQRTEELEESKKKL--AQR-LQEAEEQIEAVNSKCASLEKTKQ--RLQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEEISERLEEAGGATSAQIEMNKKREAEFQKLRRDL---EESTLQHEATASALRKKQADS
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72; Conserv
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       Kobayashi S.,
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22.1%;
                                                                            Orii H.;
the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 173.5; DB; Pred. No. 0.092; 67; Mismatches 1
     Orii H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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     Agata
                                                                                                                                                                                                                                  Turbellaria;
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     ×;
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                                                                              databases
     Watanabe
                                                                                                                                                                                                                                  Seriata;
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DT 0.
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Best Local Similarity
Matches 94; Conserv
                           Q9AMC4;
01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                  Q9AMC4
                                                                                                                                                   1163 KSNSQGTGGVRSEEM----EEFKRKMNARIQELEEESESNKSKCSQLEKVKSRLQG
                                                                                                                                                                                                            1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000355; myosin_head; 1.

SMART; SM00215; IQ: 1.

SMART; SM00242; MYSC; 1.

PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.

PROSITE; PS00182; GLNA_ADENYLATION; UNKNOWN_1.

PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                1072
                                                                                                                                                                                                                                                                                                                      1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head;
Pfam; PF01576; Myosin_tail;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of two distinct muscles in the planarian, Dug-
japonica, by the expression of myosin heavy chain genes.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: BELONGS TO THE GNTR FAMILY OF TRANSCRIPTIONAL
              M18 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
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                                                                                                                                                                                                                                                                QHENSELHKSLEDAESQINQLSKAKQQLQAQL-----EEAKQNLEDESRAKSKLNGDLR
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PR00193; MYOSINHEAVY
PR00194; TROPOMYOSIN
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IPR001637; GlnA_adenyltn.
IPR000524; HTH_GntR.
                            (TrEMBLrel.
                                         (TrEMBLrel. (TrEMBLrel.
                                                                                 PRELIMINARY;
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Myosin_tail.
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                         Created)
Last sequence update)
Last annotation update)
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Pred. No. 0.17;
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RESULT
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1D 099MII
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Best Local
                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Eshaghi M., Manaf A., Yusoff K., Jamal F.;
Eshaghi M., Manaf A., Yusoff K., Jamal F.;
"Sequence Analysis of the 5' Region of the emm
Streptococci Isolates from Malaysia.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ
EMBL; AF326566; AAK11617.1;
InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003345; M_repeat.
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ EMBL; AF340029; AAK26382.1; -. InterPro; IPR002017; Spectrin. SEQUENCE 1120 AA; 128330 MW; A542B526FAEDF
                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TIEMBLIE). 17, Created)
01-JUN-2001 (TIEMBLIE). 17, Last sequence up
01-DEC-2001 (TIEMBLIE). 19, Last annotation
RAB6-INTERACTING PROTEIN 2 ISOFORM B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0015; GPOSANCHOR.

PROSITE; PS00343; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00746; Gram_pos_anchor; 1.
Pfam; PF02370; M; 9.
                                                                                                                                                                                                                                                                                                                                                                                       Q99MI1;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q99MI1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane SEQUENCE 43
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                                                                                                   Rab6
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                    "Characterization of
                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEKSHSPIQDVPKKICKGPRKESQLSLGGQSCAGEP
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                                                                                                                    Janoueix-Lerosey I., ization of a novel in
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Pred. No. 0
                                                                                                                       interaction
                                                                                                                                                                                                                                       Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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; Murinae; Mus
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                                                                                                                       GTPase
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01-MAY-1999
01-MAY-1999
01-DEC-2001
                                                                                                                                                                       Thyroid Hormone-induced Metamorphosing Dev. Genet. 0:0-0(1999).
EMBL; AF097905; AAD13770.1; -.
                                                                                                                                     InterPro; IPR002928; Myosin_tail.
InterPro; IPR000533; Tropomyosin.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                         TISSUE-TAIL MUSCLE, HINDLIMB MUSCLE;
Hu H., Merrifield P., Atkinson B.G.;
"Expression of the Myosin Heavy Chain
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; V
Amphibia; Batrachia; Anura; Neobatrachia;
                                                                                                                                                                                                                                                                                                                    MHC-2
                                                                                                                                                                                                                                                                                                                               MYOSIN HEAVY CHAIN
                                                                                                                                                                                                                                                                                                                                                                                       Q9YHD7
                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                        Rana catesbeiana (Bull frog).
                                                                                                     SEQUENCE
                                                                                                                             PRINTS;
                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERVKSLQADTTNTDTALTTLEEALADKERTIERLK-----EQRDRDEREKQEEIDTYKK
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                    TCPQCRIQVGKRTIINKLFFDLAQEEENVLD-----REFLKNELDNVRAQLSQKDKEK--
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TTQRARLQTENGELSRQL----
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                                            l Similarity
93; Conserv
                                                                                                                          PR00194;
                                                                                                    708 AA;
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(TrEMBLrel. 10, Last
(TrEMBLrel. 19, Last
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                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                               N.A.
                                                                                                                           TROPOMYOSIN
                                                                                                                                                                                                                                                                                                                              (FRAGMENT).
                                                                                                     81824 MW;
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                                                     7.28;
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                                             83;
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                                                                                                                                                                                                                                                                                                                                                                Created)
EEKESLISQLSRGKLGFTQQVEELKRQLEEESKAKNA 101
                                                    Score 172.5; DB Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 173;
Pred. No. 0.
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annotation update)
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a; Ranoidea;
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                                                                   13;
                                                                                                      CRC64;
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                                                                Length
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Ranidae; Rana
                                                                                                                                                                                                           Muscle
                                                                                                                                                                                                Tadpoles.";
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                                                                   708
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392	334	336	278	276	240	217	198	160	146	102	98
392 EGDLNELEIQLSHANRQASEAQKQLRNVQGQLKDTQLHL-DDAVRGQED 439	HGYYEKLCLEKSHSPIQDVPKKICKGPRKESQLSLGGQSCAGEPD 378	LELNQIKSE-VDRKIAEKDEEIEQLKRNSQRAIDTMQSTLDSEIRSRNDALRLKKKM 391	278 LNLPPVASETVDRLVLESPAPVEVNLKLRRPSFRDDIDLNATFDVDTPPARPSSSQ 333	276 KNLQQEISDLTEQIGENGKSINELEKARKQVEQEKSDLQAALEEAEGSLEHEEAKILRVQ 335	YSELDQAKLELKSAQKDLQSADKEIM-SLK-KKLTMLQET 277	217 KKQRNFDKVLVEWKQKYEEGQAELEASQKEARSLSTEIF-KLKNSYEEALEQVETLKREN 275	AVYCVSLKKEYENLKEARKASGEVADKLRKDLFSSRSKLQTV 239	EDAKKKLAQRLQDAEEQVEAVNSKCGSLEKTKQRLQSEVEDLMVDVERANGAAAALD 216	146 QDETKQAQEEAGRLRSKMKTMEQIELLLQSQLPEVEEMIRDMGVGQSAVEQL- 197	102 LAHALQSSRHDNDLLREQYEEEQEAKAELQRSLSKANGEVAQWRTKYETDAIQRTEEL 159	VATVVSLQQALGKAEMLCSTI

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